Seminario Dott. Graziano Lolli Dipartimento di Scienze Chimiche, Università di Padova 15 gennaio 2015, ore 15:00 - Chiostro di S. Maria delle Grazie, Aula F4

"Protein crystallography at a glance"

To celebrate the centennial of Bragg's first X-ray diffraction from crystals, UNESCO declared 2014 the "International Year of Crystallography". The UN resolution points out that crystallography is a fundamental technique serving many disciplines in a very fertile manner as documented by 23 Nobel Prizes awarded in the area, the last in 2012.

Protein Crystallography has a shorter history starting from the structures of myoglobin and haemoglobin (Kendrew & Perutz, Nobel Prize 1962). In the last 50 years it has been used to understand the molecular details of protein functions and malfunctions, to define enzymatic mechanisms, to develop new drugs, to rationally engineering new protein functions and much more.

A few examples will be used to highlight the role of crystallography in defining regulatory mechanisms of protein kinases in cell cycle and transcription (CDKs and CK2) and the function of the prestin protein in the mammalian earing process. Structure-based drug design will be illustrated for the development of kinase inhibitors as potential cancer treatment. New methodologies and still developing technologies, such as fragment-based drug discovery and X-ray Free Electron Laser (X-FEL), are expected to significantly boost new therapeutic approaches (interference with protein-protein interactions as in the case of bromodomains) as well as our structural understanding of more challenging systems (i.e. membrane proteins).